RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/828,574

DATE: 02/26/2002
TIME: 11:09:41

Input Set : A:\UCSD1310-1.ST25.txt
Output Set: N:\CRF3\02262002\I828574.raw

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 2 <110> APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 3         ALBANI, Salvatore
 4         PRAKKEN, Berent J.
 6 <120> TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
 8 <130> FILE REFERENCE: UCSD1310-1
10 <140> CURRENT APPLICATION NUMBER: US 09/828,574
11 <141> CURRENT FILING DATE: 2001-04-06
13 <150> PRIOR APPLICATION NUMBER: US 60/224,104
14 <151> PRIOR FILING DATE: 2000-08-09
16 <160> NUMBER OF SEQ ID NOS: 13
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 573
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens
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28 1               5                   10                  15
31 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
32              20                  25                  30
35 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
36          35                  40                  45
39 Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
40          50                  55                  60
43 Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
44 65                  70                  75                  80
47 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
48                  85                  90                  95
51 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly
52              100                 105                 110
55 Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe
56          115                 120                 125
59 Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
60      130                 135                 140
63 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
64 145                 150                 155                 160
67 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
68              165                 170                 175
71 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
72          180                 185                 190
75 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
76      195                 200                 205
79 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
```

```
80     210                        215                     220
83 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
84 225                    230                235                 240
87 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
88                    245                250                255
91 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
92              260                265                270
95 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
96          275                280                285
99 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
100    290                295                300
103 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
104 305                310                315                 320
107 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
108                325                330                335
111 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
112            340                345                350
115 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu
116          355                360                365
119 Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
120    370                375                380
123 Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
124 385                390                395                 400
127 Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
128                405                410                415
131 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
132            420                425                430
135 Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile
136          435                440                445
139 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
140    450                455                460
143 Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
144 465                470                475                 480
147 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
148                485                490                495
151 Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
152            500                505                510
155 Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
156          515                520                525
159 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
160    530                535                540
163 Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
164 545                550                555                 560
167 Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
168            565                570
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 15
173 <212> TYPE: PRT
174 <213> ORGANISM: Mycobacterium
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176  <400> SEQUENCE: 2
178  Gly Glu Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr
179  1               5                   10                  15
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183  <211> LENGTH: 15
184  <212> TYPE: PRT
185  <213> ORGANISM: Homo sapiens
187  <400> SEQUENCE: 3
189  Gly Glu Ala Leu Ser Thr Leu Val Leu Asn Arg Leu Lys Val Gly
190  1               5                   10                  15
193  <210> SEQ ID NO: 4
194  <211> LENGTH: 15
195  <212> TYPE: PRT
196  <213> ORGANISM: Mycobacterium
198  <400> SEQUENCE: 4
200  Pro Tyr Ile Leu Leu Val Ser Ser Lys Val Ser Thr Val Lys Asp
201  1               5                   10                  15
204  <210> SEQ ID NO: 5
205  <211> LENGTH: 15
206  <212> TYPE: PRT
207  <213> ORGANISM: Homo sapiens
209  <400> SEQUENCE: 5
211  Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
212  1               5                   10                  15
215  <210> SEQ ID NO: 6
216  <211> LENGTH: 15
217  <212> TYPE: PRT
218  <213> ORGANISM: Mycobacterium
220  <400> SEQUENCE: 6
222  Glu Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys
223  1               5                   10                  15
226  <210> SEQ ID NO: 7
227  <211> LENGTH: 15
228  <212> TYPE: PRT
229  <213> ORGANISM: Homo sapiens
231  <400> SEQUENCE: 7
233  Lys Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys
234  1               5                   10                  15
237  <210> SEQ ID NO: 8
238  <211> LENGTH: 15
239  <212> TYPE: PRT
240  <213> ORGANISM: Mycobacterium
242  <400> SEQUENCE: 8
244  Ile Ala Gly Leu Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys
245  1               5                   10                  15
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249  <211> LENGTH: 15
250  <212> TYPE: PRT
251  <213> ORGANISM: Homo sapiens
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256 1
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260 <211> LENGTH: 15
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: dnaJP1 peptide
267 <400> SEQUENCE: 10
269 Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
                            5                    10                    15
270 1
273 <210> SEQ ID NO: 11
274 <211> LENGTH: 15
275 <212> TYPE: PRT
276 <213> ORGANISM: Artificial sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Irrelevant dnaJpV peptide
281 <400> SEQUENCE: 11
283 Asp Glu Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
                            5                    10                    15
284 1
287 <210> SEQ ID NO: 12
288 <211> LENGTH: 11
289 <212> TYPE: PRT
290 <213> ORGANISM: Artificial sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: pan-DR binder peptide
295 <220> FEATURE:
296 <221> NAME/KEY: MISC_FEATURE
297 <222> LOCATION: (2)..(2)
298 <223> OTHER INFORMATION: Xaa is any amino acid
300 <400> SEQUENCE: 12
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303 1                      5                    10
306 <210> SEQ ID NO: 13
307 <211> LENGTH: 573
308 <212> TYPE: PRT
309 <213> ORGANISM: Homo sapiens
311 <400> SEQUENCE: 13
313 Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg
                            5                    10                    15
314 1
317 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
                            5                    25                    30
318        20
321 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
                                            40                    45
322        35
325 Asp Ala Val Ala Val Thr Met Glu Pro Lys Gly Arg Thr Val Ile Ile
                                            55                    60
326        50
329 Glu Gln Ser Trp Gly Ser Pro Asn Val Thr Lys Asp Gly Val Thr Val
                                            70                    75                    80
330 65
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PATENT APPLICATION·   US/09/828,574

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333 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
334             85              90              95
337 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ser Gly Asp Gly
338             100             105             110
341 Thr Thr Thr Ala Thr Val Leu Ala Gly Ser Ile Ala Lys Glu Gly Phe
342             115             120             125
345 Gln Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
346         130             135             140
349 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
350 145             150             155             160
353 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Met Ile Ser Ala
354             165             170             175
357 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
358             180             185             190
361 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
362         195             200             205
365 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
366         210             215             220
369 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
370 225             230             235             240
373 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Val Gln Ser
374             245             250             255
377 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His His Lys Pro Leu Val
378             260             265             270
381 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Ile Leu
382         275             280             285
385 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
386     290             295             300
389 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
390 305             310             315             320
393 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
394             325             330             335
397 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
398             340             345             350
401 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Leu Glu
402         355             360             365
405 Lys Arg Ile Gln Glu Ile Ile Gly Gln Leu Asp Val Thr Thr Ser Glu
406     370             375             380
409 Tyr Glu Lys Glu Lys Leu Asn Glu Trp Leu Ala Lys Leu Ser Asp Gly
410 385             390             395             400
413 Val Val Val Leu Lys Phe Gly Gly Thr Ser Asp Val Glu Val Asn Glu
414             405             410             415
417 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
418         420             425             430
421 Glu Gly Gly Ile Val Leu Gly Gly Gly Phe Ala Leu Leu Arg Cys Ile
422         435             440             445
425 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
426     450             455             460
429 Met Glu Ile Val Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Thr Ala
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VERIFICATION SUMMARY   DATE: 02/26/2002
PATENT APPLICATION: **US/09/828,574**   TIME: 11:09:42

Input Set : **A:\UCSD1310-1.ST25.txt**
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L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12